Figure 1

```
ATATTGCTGAGCTCAGGGAGTGAGGGCCCCACATTTGAGACAGTGAGCCCCAAGAAGAGG   60

GATCCCTGCTCCAGCAGCTGCAAGGTGCAAGAAGAAGAAGATCCCAGGGAGGAAAATGTG  120
                                                    M  C          2

CTGGAGACCCCTGTGTCGGTTCCTGTGGCTTTGGTCCTATCTGTCTTATGTTCAAGCAGT  180
W  R  P  L  C  R  F  L  W  L  W  S  Y  L  S  Y  V  Q  A  V     22

GCCTATCCAGAAAGTCCAGGATGACACCAAAACCCTCATCAAGACCATTGTCACCAGGAT  240
P  I  Q  K  V  Q  D  D  T  K  T  L  I  K  T  I  V  T  R  I     42

CAATGACATTTCACACACGCAGTCGGTATCCGCCAAGCAGAGGGTCACTGGCTTGGACTT  300
N  D  I  S  H  T  Q  S  V  S  A  K  Q  R  V  T  G  L  D  F     62

CATTCCTGGGCTTCACCCCATTCTGAGTTTGTCCAAGATGGACCAGACTCTGGCAGTCTA  360
I  P  G  L  H  P  I  L  S  L  S  K  M  D  Q  T  L  A  V  Y     82

TCAACAGGTCCTCACCAGCCTGCCTTCCCAAAATGTGCTGCAGATAGCCAATGACCTGGA  420
Q  Q  V  L  T  S  L  P  S  Q  N  V  L  Q  I  A  N  D  L  E    102

GAATCTCCGAGACCTCCTCCATCTGCTGGCCTTCTCCAAGAGCTGCTCCCTGCCTCAGAC  480
N  L  R  D  L  L  H  L  L  A  F  S  K  S  C  S  L  P  Q  T    122

CAGTGGCCTGCAGAAGCCAGAGAGCCTGGATGGCGTCCTGGAAGCCTCACTCTACTCCAC  540
S  G  L  Q  K  P  E  S  L  D  G  V  L  E  A  S  L  Y  S  T    142

AGAGGTGGTGGCTTTGAGCAGGCTGCAGGGCTCTCTGCAGGACATTCTTCAACAGTTGGA  600
E  V  V  A  L  S  R  L  Q  G  S  L  Q  D  I  L  Q  Q  L  D    162

TGTTAGCCCTGAATGCTGAAGTTTCAAAGGCCACCAGGCTCCCAAGAATCATGTAGAGGG  660
V  S  P  E  C  *                                               167

AAGAAACCTTGGCTTCCAGGGGTCTTCAGGAGAAGAGAGCCATGTGCACACATCCATCAT  720

TCATTTCTCTCCCTCCTGTAGACCACCCATCCAAAGGCATGACTCCACAATGCTTGACTC  780

AAGTTATCCACACAACTTCATGAGCACAAGGAGGGGCCAGCCTGCAGAGGGGACTCTCAC  840

CTAGTTCTTCAGCAAGTAGAGATAAGAGCCATCCCATCCCCTCCATGTCCCACCTGCTCC  900

GGGTACATGTTCCTCCGTGGGTACACGCTTCGCTGCGGCCCAGGAGAGGTGAGGTAGGGA  960

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CGCTCAAGATTGACCTCTGGTGACTGGTTTTGTTTCTATTGTGACTGACTCTATCCAAAC 1320

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TCCAGCCAGGTCATACCCTGTGGAGGTGAGCGGGATCAGGTTTTGTGGTGCTAAGAGAGG 2820

AGTTGGAGGTAGATTTTGGAGGATCTGAGGGC                               2852
```

Figure 2

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GTCCAAGCTG TGCCCATCCA AAAAGTCCAA GATGACACCA AAACCCTCAT     150
CAAGACAATT GTCACCAGGA TCAATGACAT TTCACACACG CAGTCAGTCT     200
CCTCCAAACA GAAAGTCACC GGTTTGGACT TCATTCCTGG GCTCCACCCC     250
ATCCTGACCT TATCCAAGAT GGACCAGACA CTGGCAGTCT ACCAACAGAT     300
CCTCACCAGT ATGCCTTCCA GAAACGTGAT CCAAATATCC AACGACCTGG     350
AGAACCTCCG GGATCTTCTT CACGTGCTGG CCTTCTCTAA GAGCTGCCAC     400
TTGCCCTGGG CCAGTGGCCT GGAGACCTTG GACAGCCTGG GGGGTGTCCT     450
GGAAGCTTCA GGCTACTCCA CAGAGGTGGT GGCCCTGAGC AGGCTGCAGG     500
GGTCTCTGCA GGACATGCTG TGGCAGCTGG ACCTCAGCCC TGGGTGCTGA     550
GGCCTTGAAG GTCACTCTTC CTGCAAGGAC T-ACGTTAAG GGAAGGAACT     600
CTGGTTTCCA GGTATCTCCA GGATTGAAGA GCATTGCATG GACACCCCTT     650
ATCCAGGACT CTGTCAATTT CCCTGACTCC TCTAAGCCAC TCTTCCAAAG     700
G                                                         701
```

Figure 4

```
Mouse   MCWRPLCRFL WLWSYLSYVQ AVPIQKVQDD TKTLIKTIVT RINDISHTQS     50
Human   MHWGTLCGFL WLWPYLFYVQ AVPIQKVQDD TKTLIKTIVT RINDISHTQS

Mouse   VSAKQRVTGL DFIPGLHPIL SLSKMDQTLA VYQQVLTSLP SQNVLQIAND    100
Human   VSSKQKVTGL DFIPGLHPIL TLSKMDQTLA VYQQILTSMP SRNVIQISND

Mouse   LENLRDLLHL LAFSKSCSLP QTSGLQKPES LDGVLEASLY STEVVALSRL    150
Human   LENLRDLLHV LAFSKSCHLP WASGLETLDS LGGVLEASGY STEVVALSRL

Mouse   QGSLQDILQQ LDVSPEC                                       167
Human   QGSLQDMLWQ LDLSPGC
```

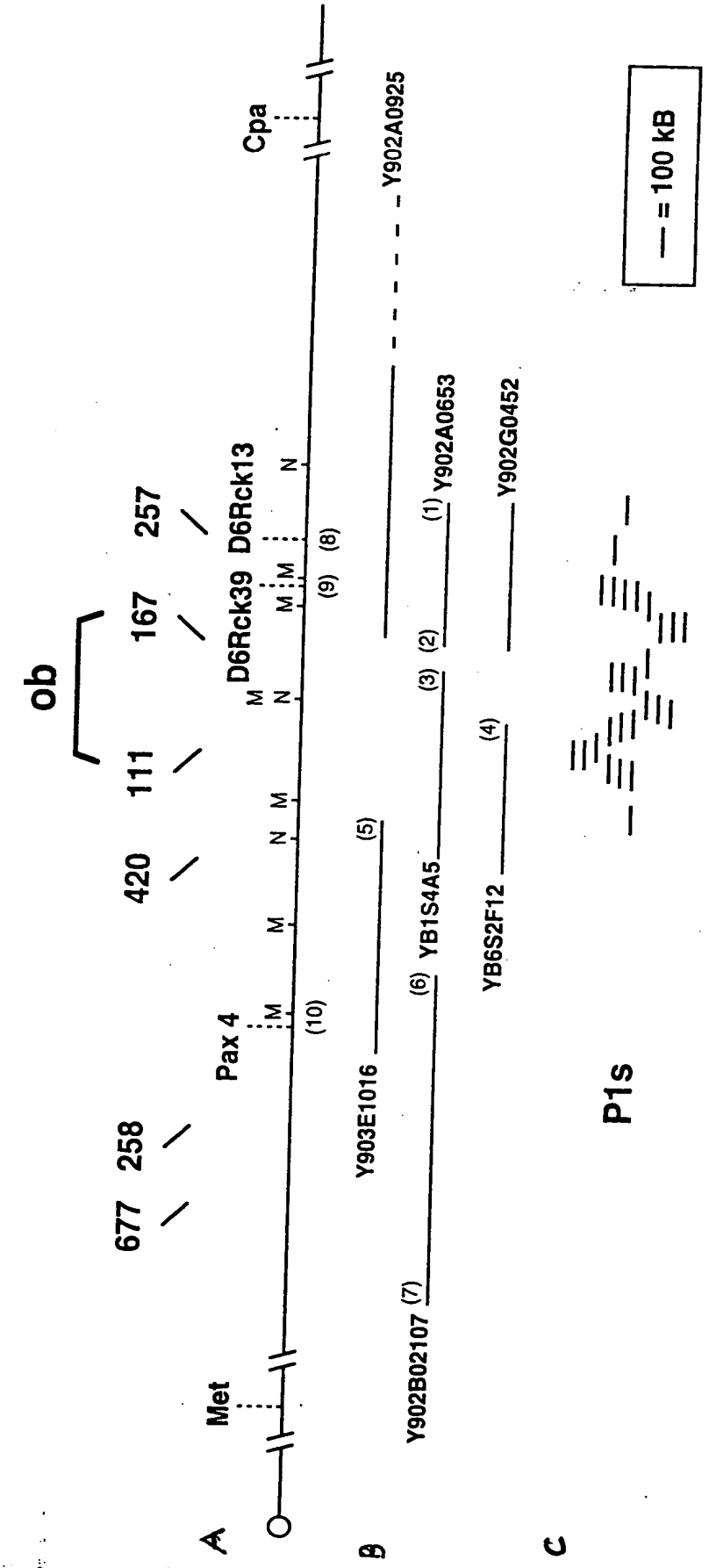
Figure 5

1	Met Cys Trp Arg Pro Leu Cys Arg Phe Leu Trp Leu Trp Ser Tyr
16	Leu Ser Tyr Val Gln Ala Val Pro Ile Gln Lys Val Gln Asp Asp
31	Thr Lys Thr Leu Ile Lys Thr Ile Val Thr Arg Ile Asn Asp Ile
46	Ser His Thr Ser Val Ser Ala Lys Gln Arg Val Thr Gly Leu Asp
61	Phe Ile Pro Gly Leu His Pro Ile Leu Ser Leu Ser Lys Met Asp
76	Gln Thr Leu Ala Val Tyr Gln Gln Val Leu Thr Ser Leu Pro Ser
91	Gln Asn Val Leu Gln Ile Ala Asn Asp Leu Glu Asn Leu Arg Asp
106	Leu Leu His Leu Leu Ala Phe Ser Lys Ser Cys Ser Leu Pro Gln
121	Thr Ser Gly Leu Gln Lys Pro Glu Ser Leu Asp Gly Val Leu Glu
136	Ala Ser Leu Tyr Ser Thr Glu Val Val Ala Leu Ser Arg Leu Gln
151	Gly Ser Leu Gln Asp Ile Leu Gln Gln Leu Asp Val Ser Pro Glu
166	Cys End

Figure 6

1	Met His Trp Gly Thr Leu Cys Gly Phe Leu Trp Leu Trp Pro Tyr
16	Leu Phe Tyr Val Gln Ala Val Pro Ile Gln Lys Val Gln Asp Asp
31	Thr Lys Thr Leu Ile Lys Thr Ile Val Thr Arg Ile Asn Asp Ile
46	Ser His Thr Ser Val Ser Ser Lys Gln Lys Val Thr Gly Leu Asp
61	Phe Ile Pro Gly Leu His Pro Ile Leu Thr Leu Ser Lys Met Asp
76	Gln Thr Leu Ala Val Tyr Gln Gln Ile Leu Thr Ser Met Pro Ser
91	Arg Asn Val Ile Gln Ile Ser Asn Asp Leu Glu Asn Leu Arg Asp
106	Leu Leu His Val Leu Ala Phe Ser Lys Ser Cys His Leu Pro Trp
121	Ala Ser Gly Leu Glu Thr Leu Asp Ser Leu Gly Gly Val Leu Glu
136	Ala Ser Gly Tyr Ser Thr Glu Val Val Ala Leu Ser Arg Leu Gln
151	Gly Ser Leu Gln Asp Met Leu Trp Gln Leu Asp Leu Ser Pro Gly
166	Cys End

Figure 7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B
C
Met
677
258
Pax 4
420
111
ob
167
257
Cpa
M
N
M
N
M
N
M
M
M
N
(10)
(9)
(8)
D6Rck39
D6Rck13
Y902A0925
Y902A0653
(1)
(2)
(3)
(4)
(5)
(6)
(7)
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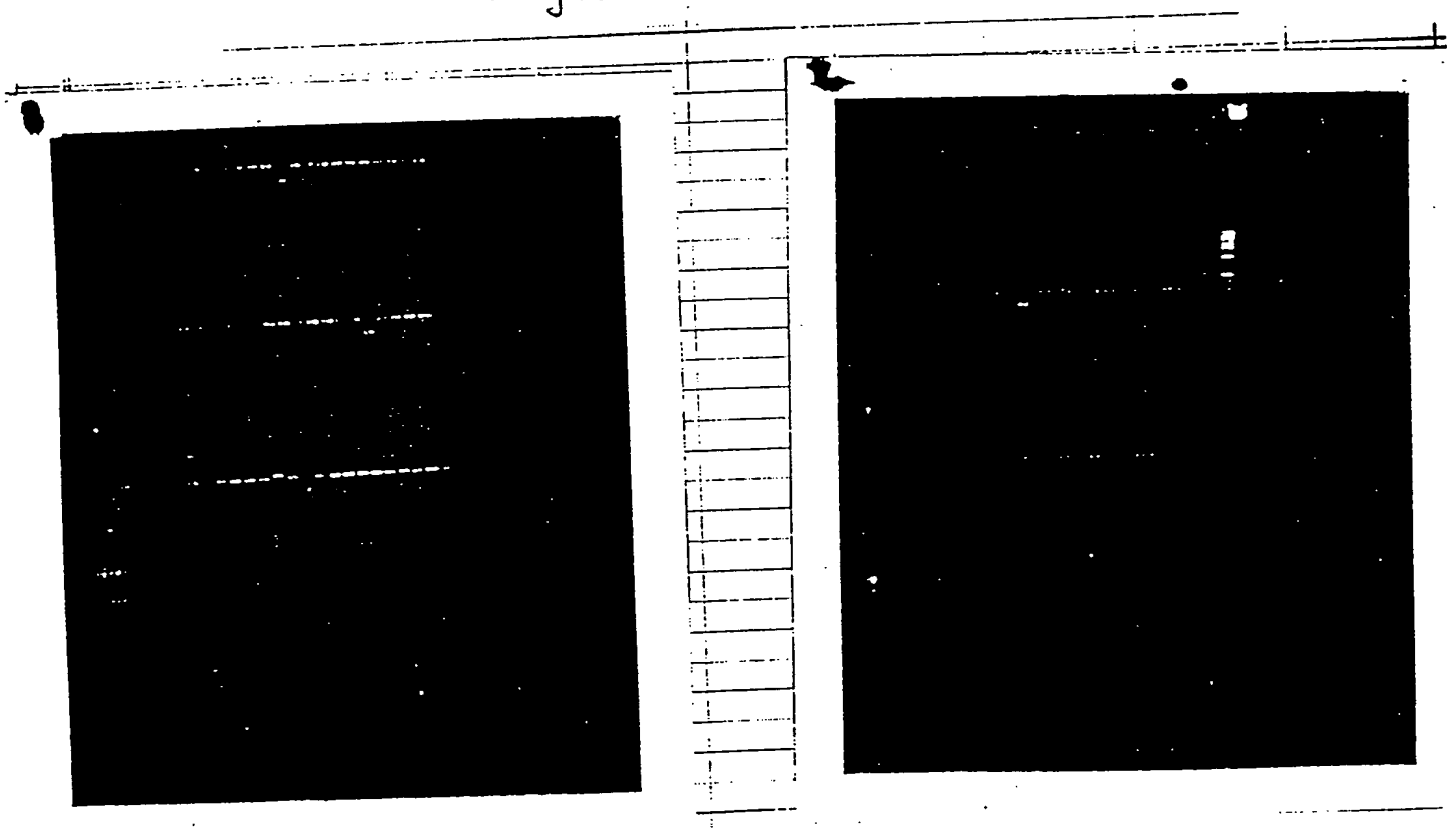
YB1S4A5
YB6S2F12
Y902G0452
Y902B02107
P1s
— = 100 kB

Figure 8



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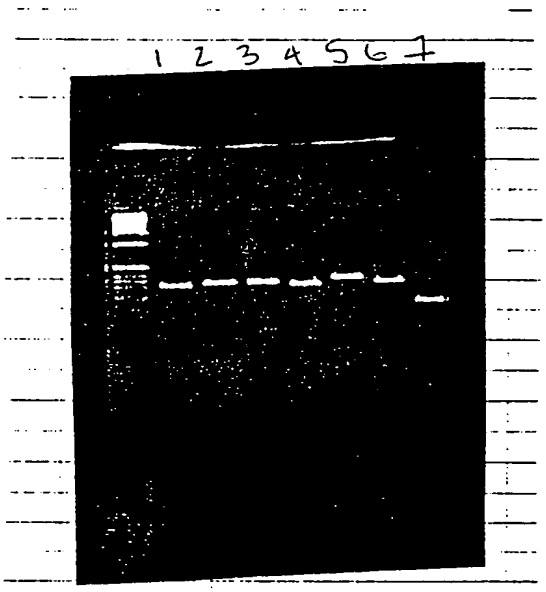

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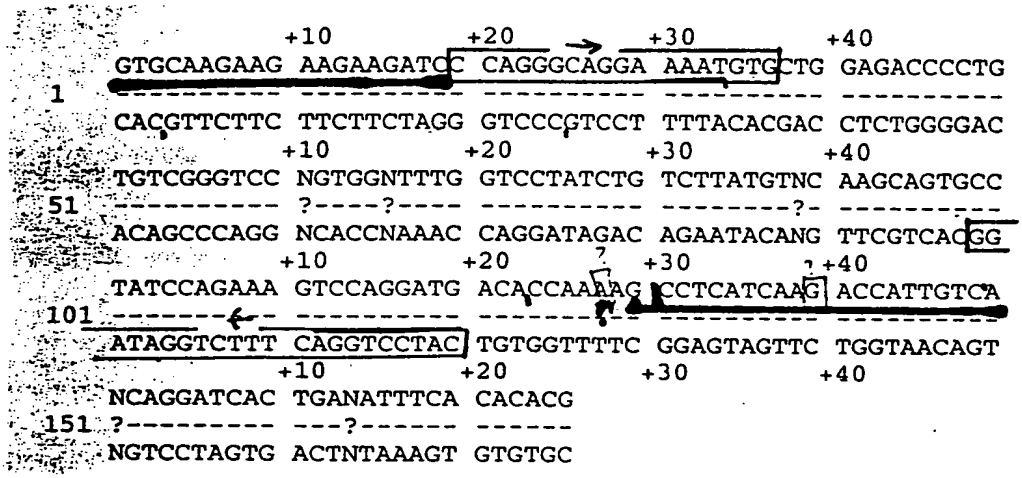
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1
CACGTTCTTC TTCTTCTAGG GTCCCGTCCT TTTACACGAC CTCTGGGGAC
+10 +20 +30 +40
TGTCGGGTCC NGTGGNTTTG GTCCTATCTG TCTTATGTNC AAGCAGTGCC
51
ACAGCCCAGG NCACCNAAAC CAGGATAGAC AGAATACANG TTCGTCACGG
+10 +20 +30 +40
TATCCAGAAA GTCCAGGATG ACACCAAAAG CCTCATCAAG ACCATTGTCA
101
ATAGGTCTTT CAGGTCCTAC TGTGGTTTTC GGAGTAGTTC TGGTAACAGT
+10 +20 +30 +40
NCAGGATCAC TGANATTTCA CACACG
151
NGTCCTAGTG ACTNTAAAGT GTGTGC

Figure 11A

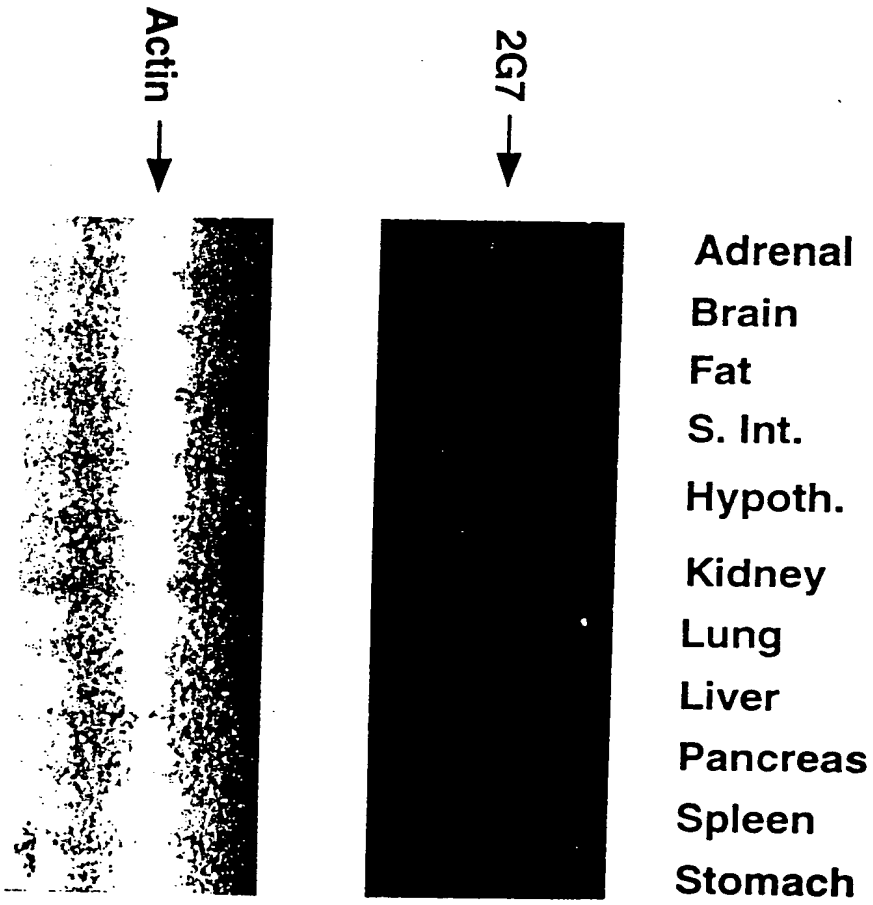

Actin
2G7
Adrenal
Brain
Fat
S. Int.
Hypoth.
Kidney
Lung
Liver
Pancreas
Spleen
Stomach

Figure 11B

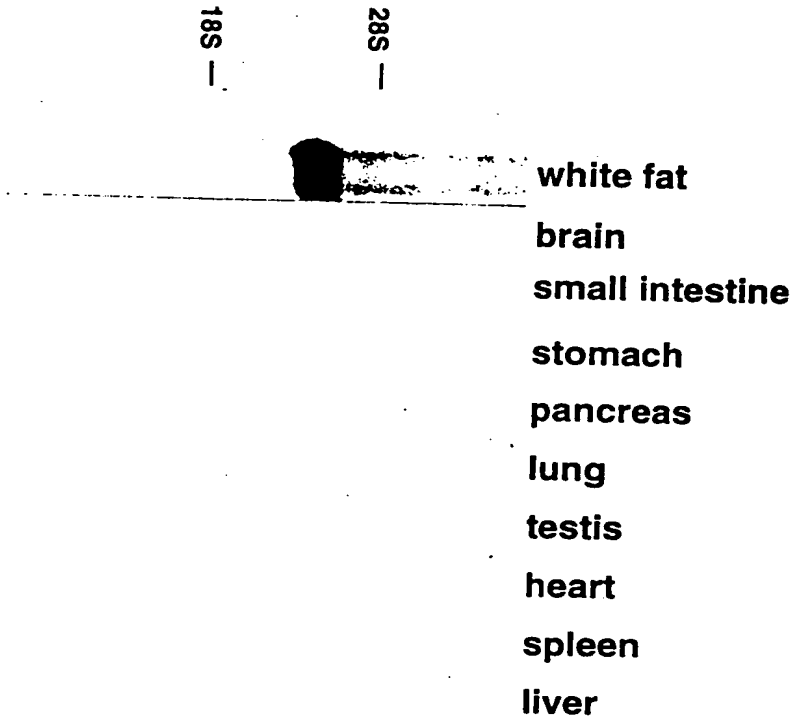

18S
28S
white fat
brain
small intestine
stomach
pancreas
lung
testis
heart
spleen
liver

Figure 12A

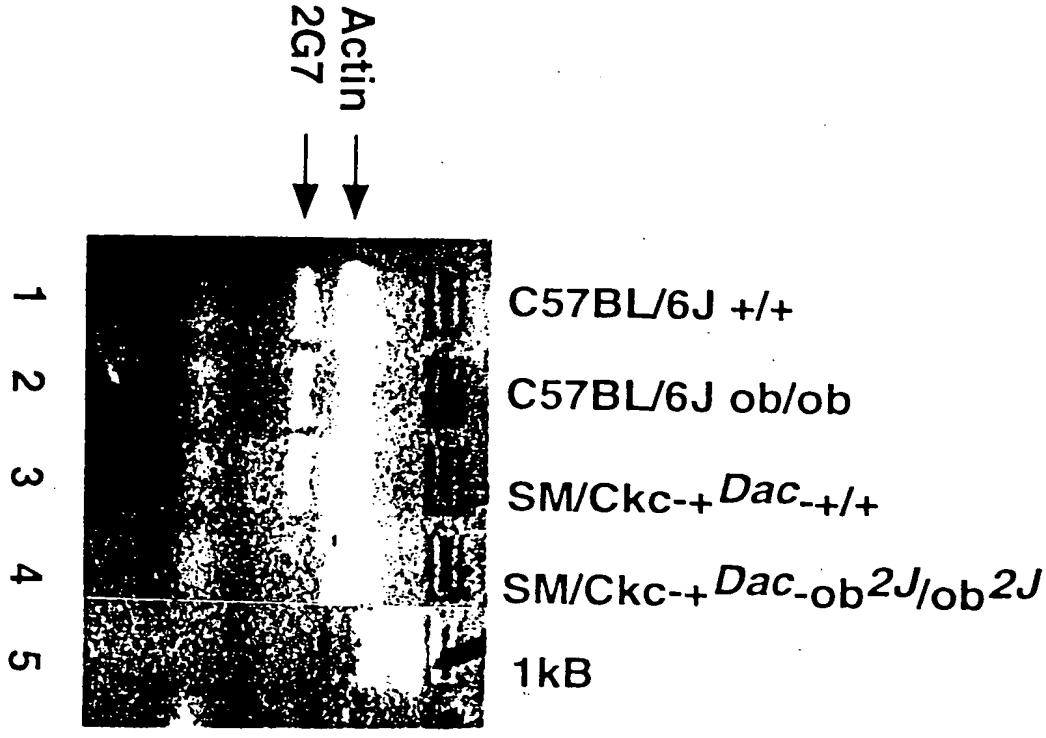

Actin
2G7
1 2 3 4 5
C57BL/6J +/+
C57BL/6J ob/ob
SM/Ckc-+Dac-+/+
SM/Ckc-+Dac-ob2J/ob2J
1kB

Figure 12 B

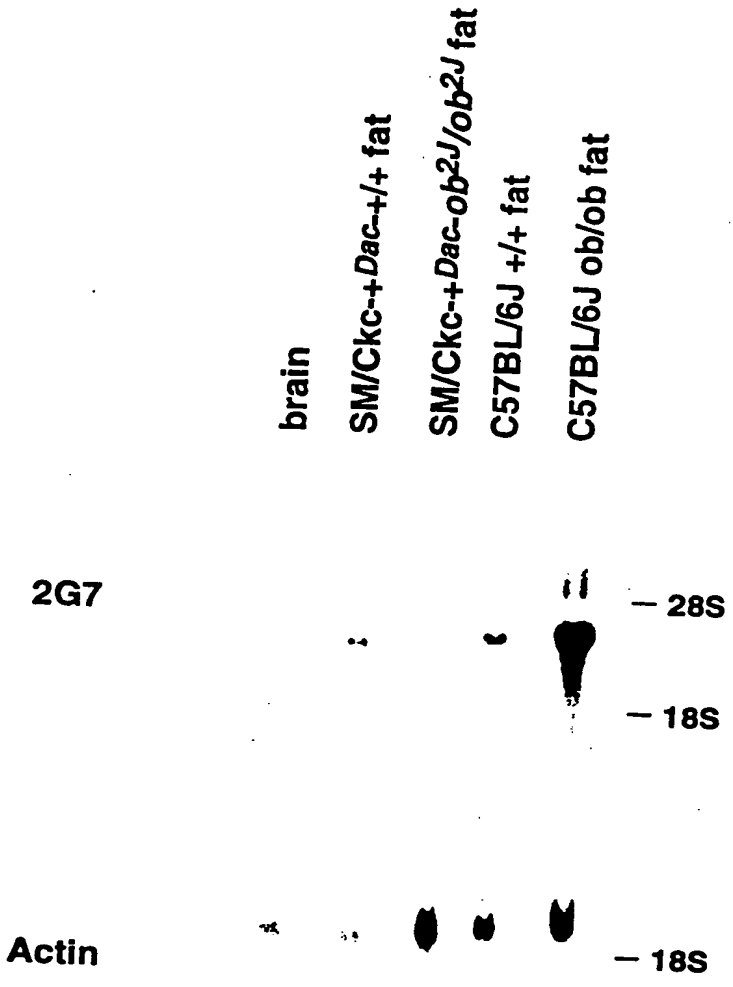

brain
SM/Ckc-+Dac-+/+ fat
SM/Ckc-+Dac-ob2J/ob2J fat
C57BL/6J +/+ fat
C57BL/6J ob/ob fat
2G7
28S
18S
Actin
18S

Figure 13

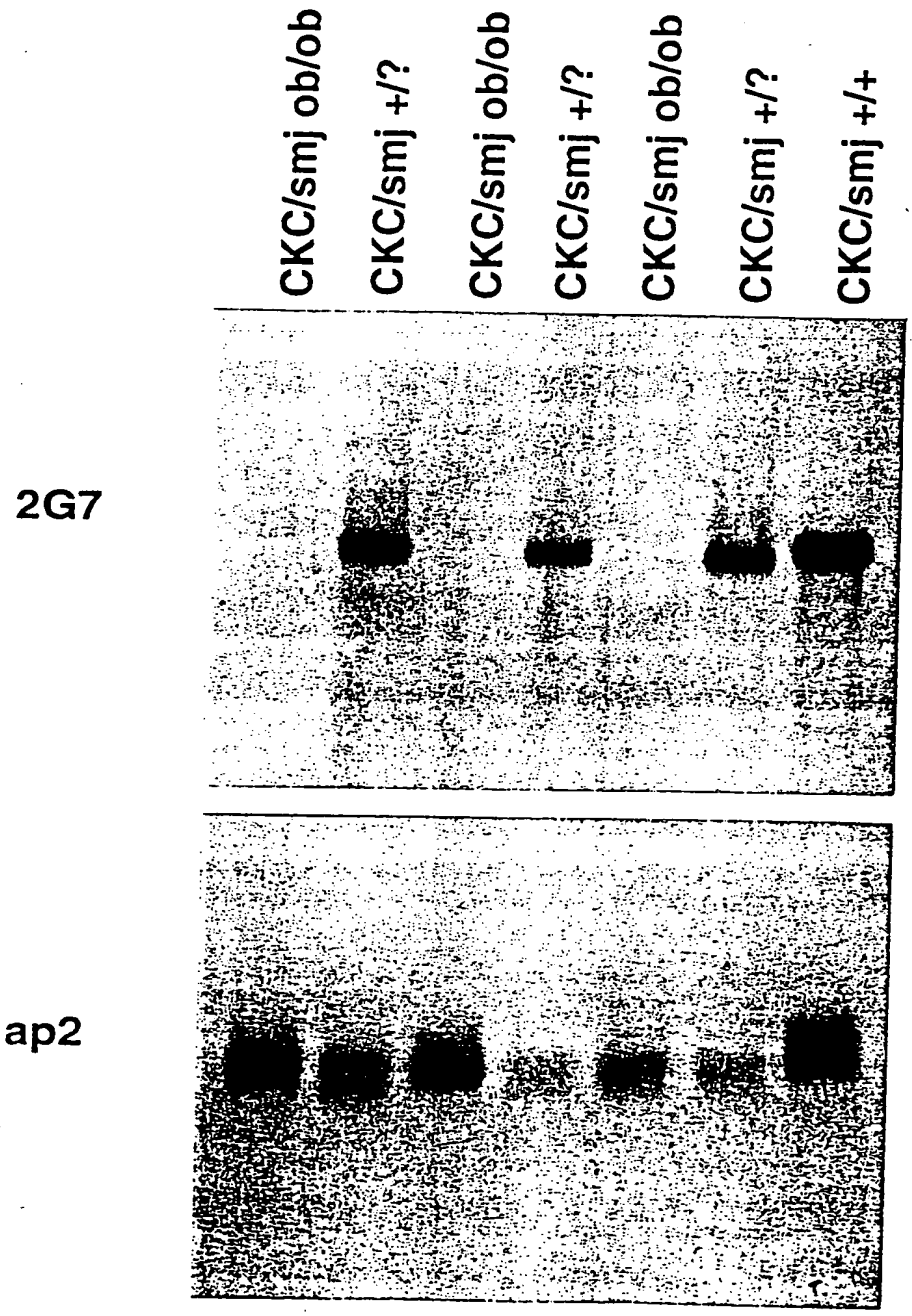
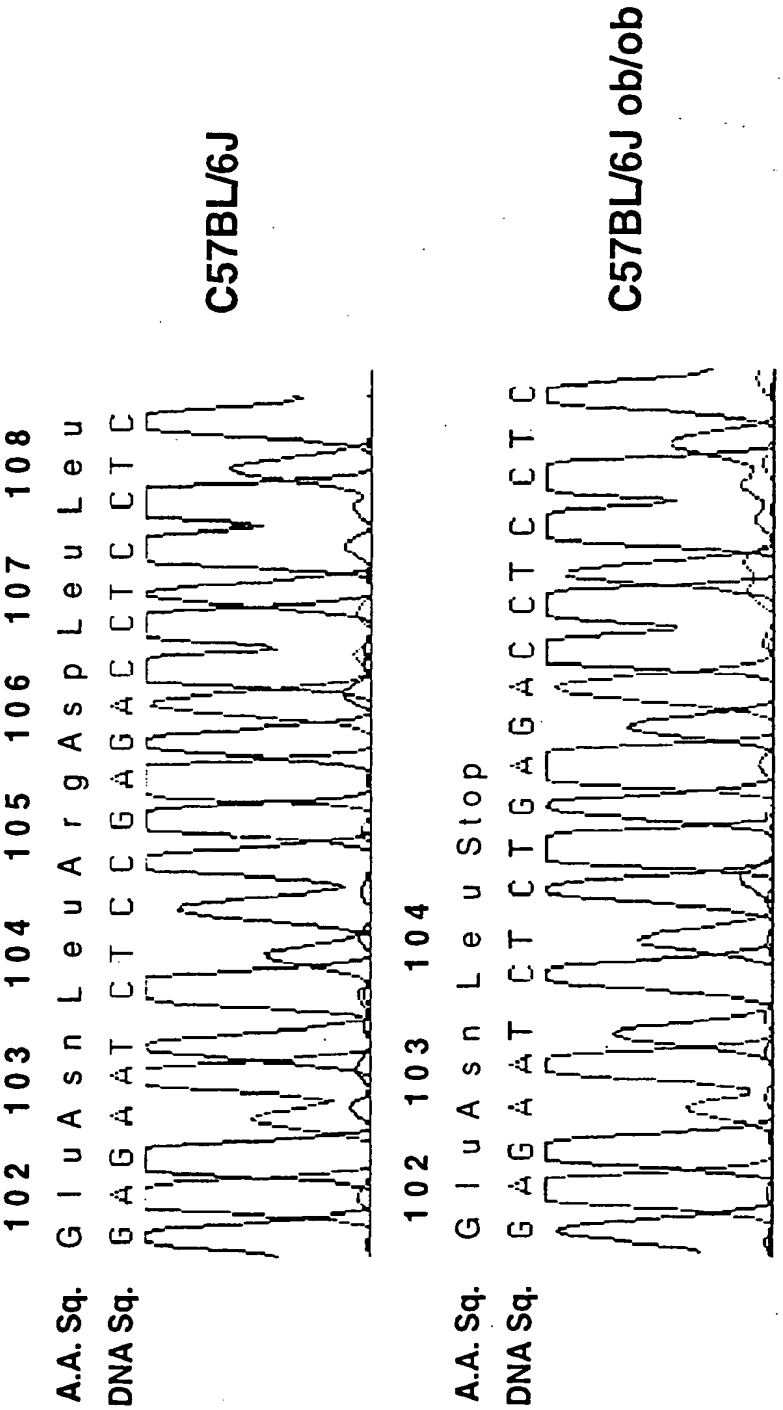

CKC/smj ob/ob
CKC/smj +/?
CKC/smj ob/ob
CKC/smj +/?
CKC/smj ob/ob
CKC/smj +/?
CKC/smj +/+
2G7
ap2

Figure 14


C57BL/6J
C57BL/6J ob/ob
A.A. Sq.
DNA Sq.
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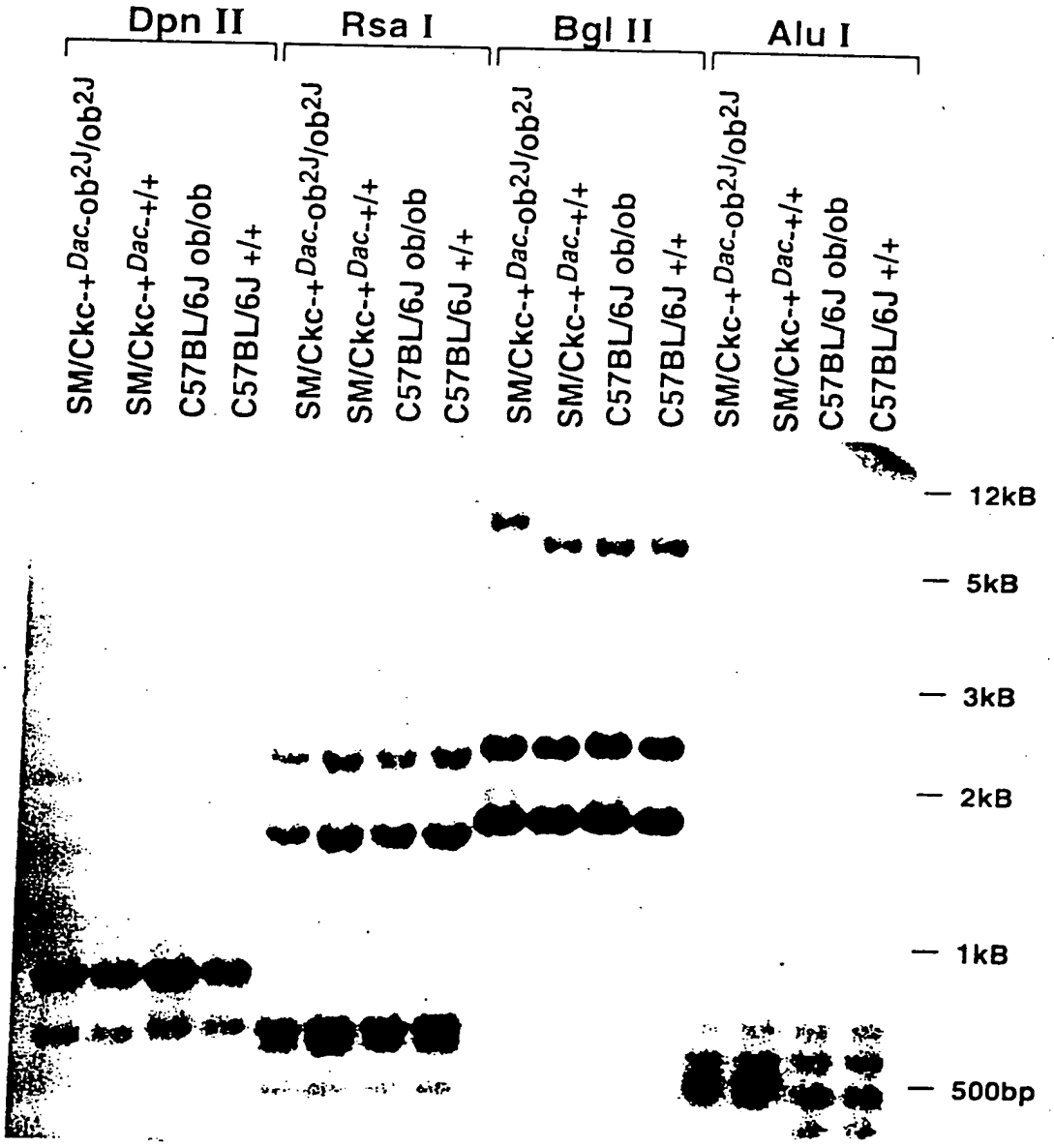
Glu Asn Leu Arg Asp Leu Leu
GAG AAT CT CCG AGA CCT CTC
A.A. Sq.
DNA Sq.
102 103 104
Glu Asn Leu Stop
GAG AAT CT CTG AGA CCT CTC

Figure 15A


Dpn II
Rsa I
Bgl II
Alu I
SM/Ckc-+Dac-ob2J/ob2J
SM/Ckc-+Dac-+/+
C57BL/6J ob/ob
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SM/Ckc-+Dac-ob2J/ob2J
SM/Ckc-+Dac-+/+
C57BL/6J ob/ob
C57BL/6J +/+
SM/Ckc-+Dac-ob2J/ob2J
SM/Ckc-+Dac-+/+
C57BL/6J ob/ob
C57BL/6J +/+
SM/Ckc-+Dac-ob2J/ob2J
SM/Ckc-+Dac-+/+
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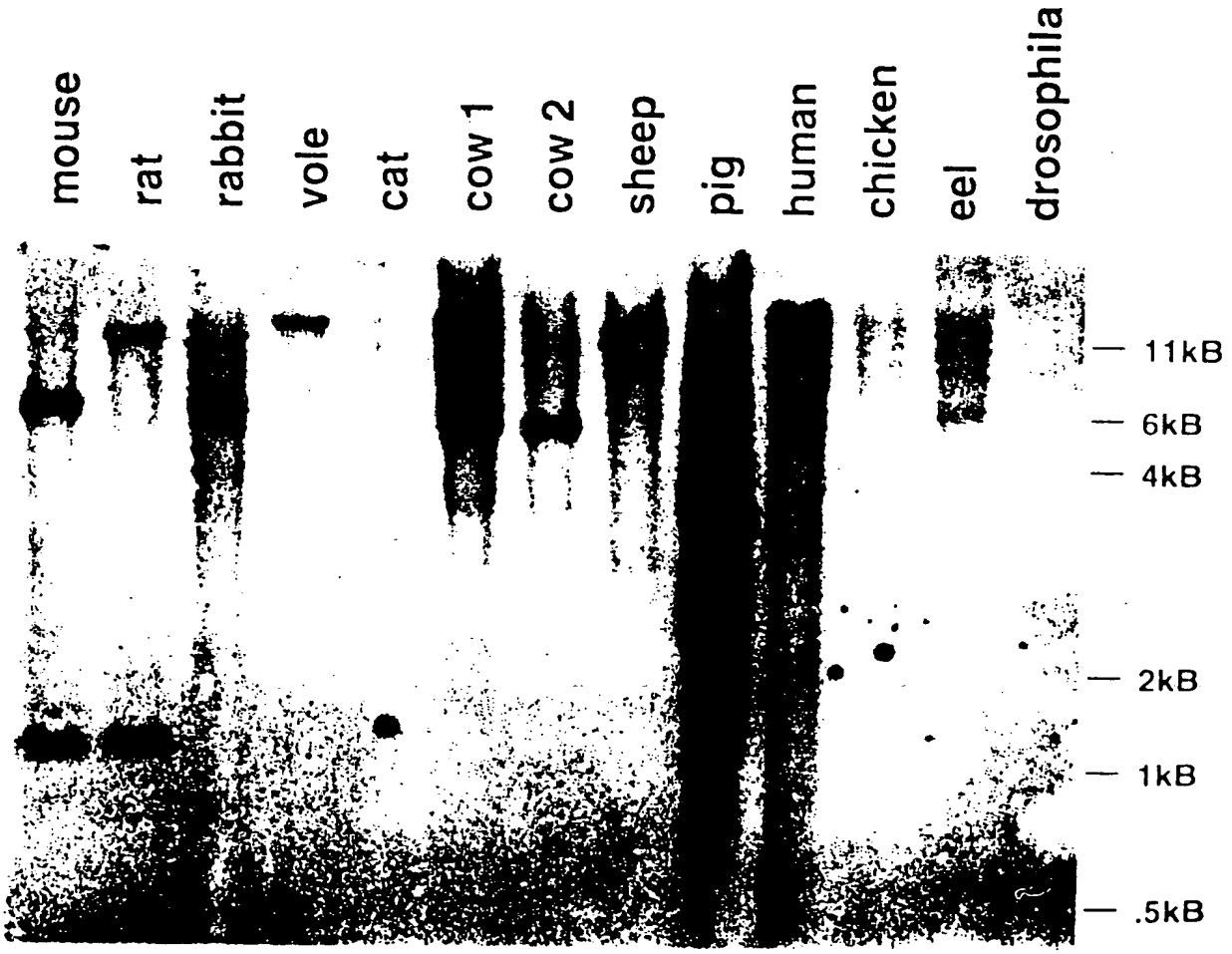
C57BL/6J +/+
12kB
5kB
3kB
2kB
1kB
500bp

Figure 16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rat
rabbit
vole
cat
cow 1
cow 2
sheep
pig
human
chicken
eel
drosophila
11kB
6kB
4kB
2kB
1kB
.5kB

Figure 15B

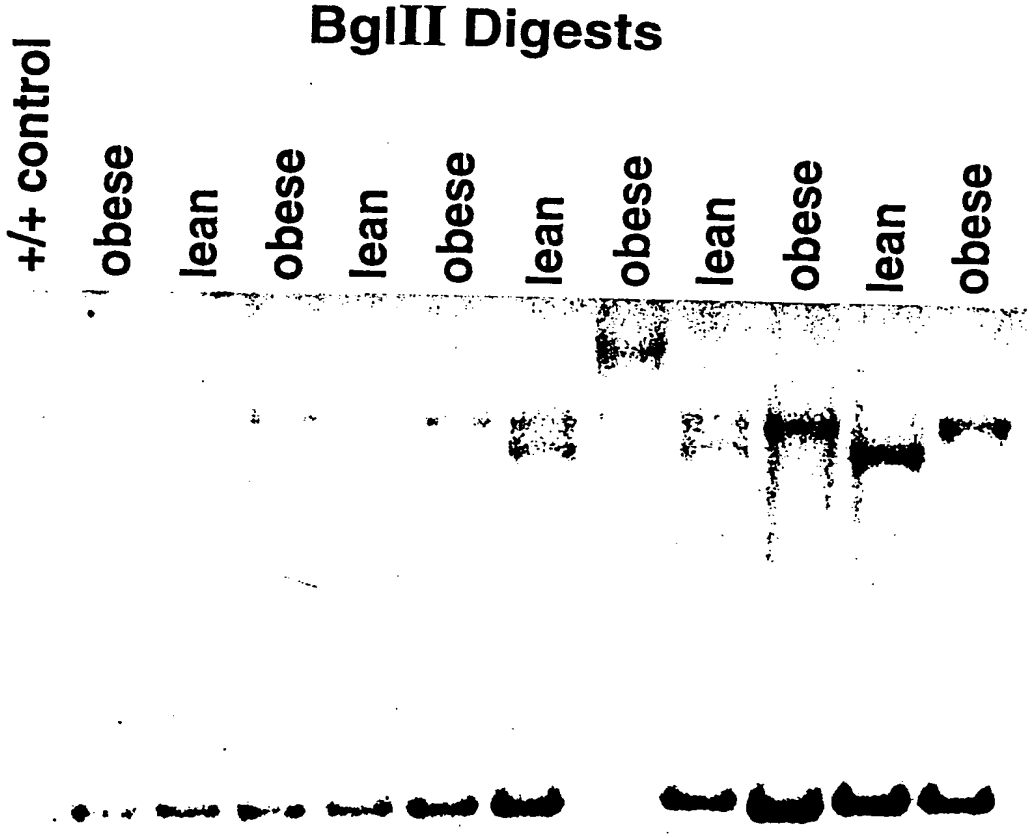
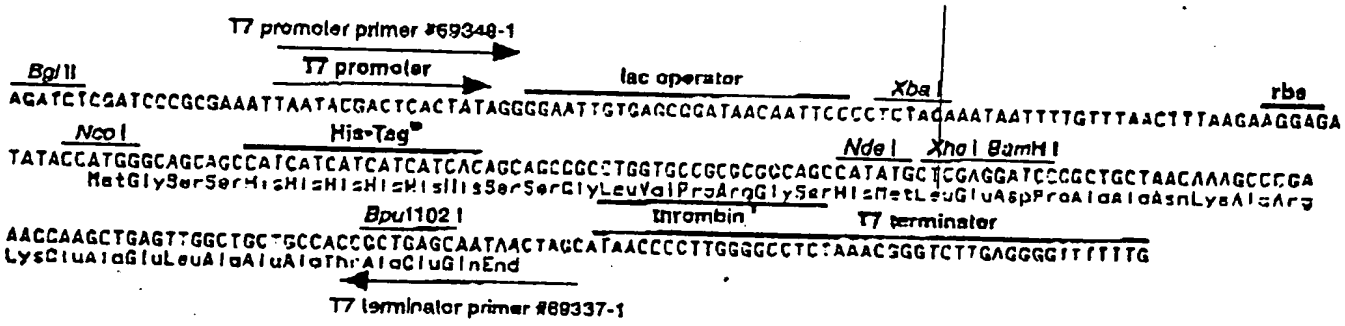

BglII Digests
+/+ control
obese
lean
obese
lean
obese
lean
obese
lean
obese
lean
obese

Figure 17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T7 promoter
lac operator
Bgl II
Xba I
rbs
Nco I
His-Tag
Nde I
Xho I BamH I
Bpu1102 I
thrombin
T7 terminator
T7 terminator primer #69337-1

Figure 18A

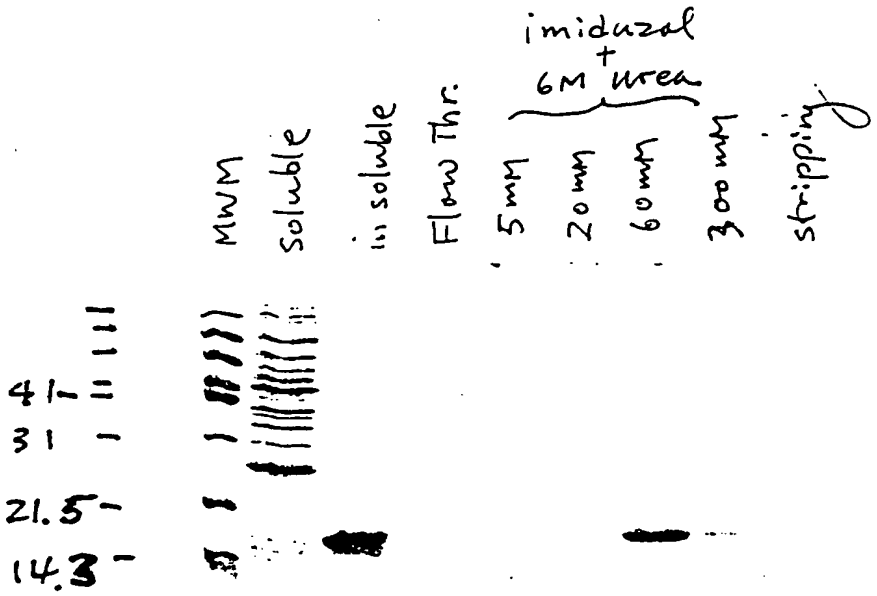
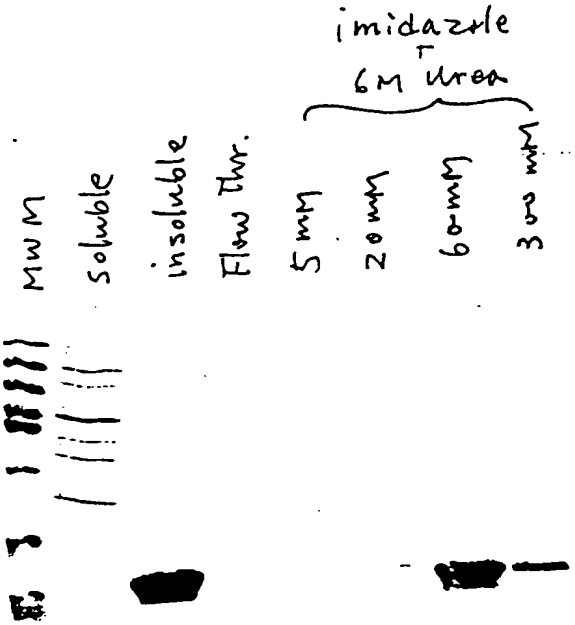

MWM
Soluble
insoluble
Flow Thr.
imidazol + 6M urea
5mM
20mM
60mM
300mM
stripping
41
31
21.5
14.3

Figure 18B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6M urea
MWM
soluble
insoluble
Flow Thr.
5mM
20mM
60mM
300mM

Figure 19A

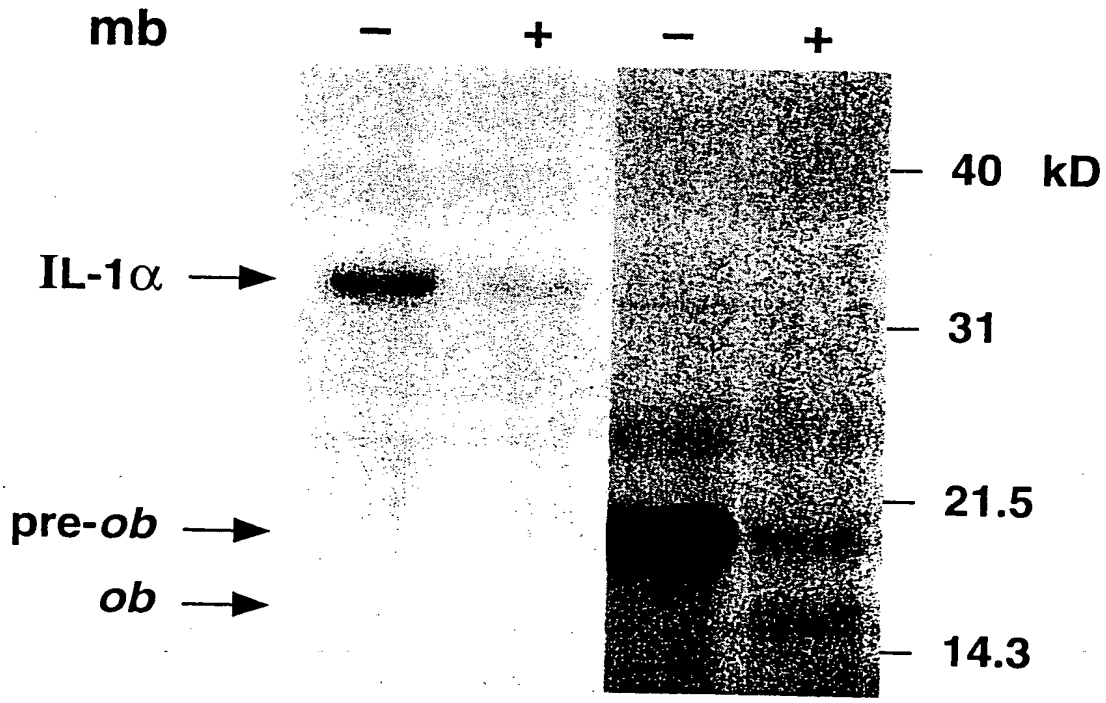


Figure 19B

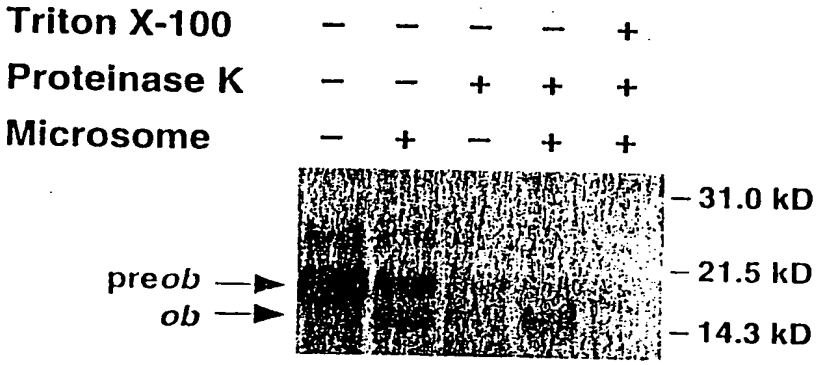
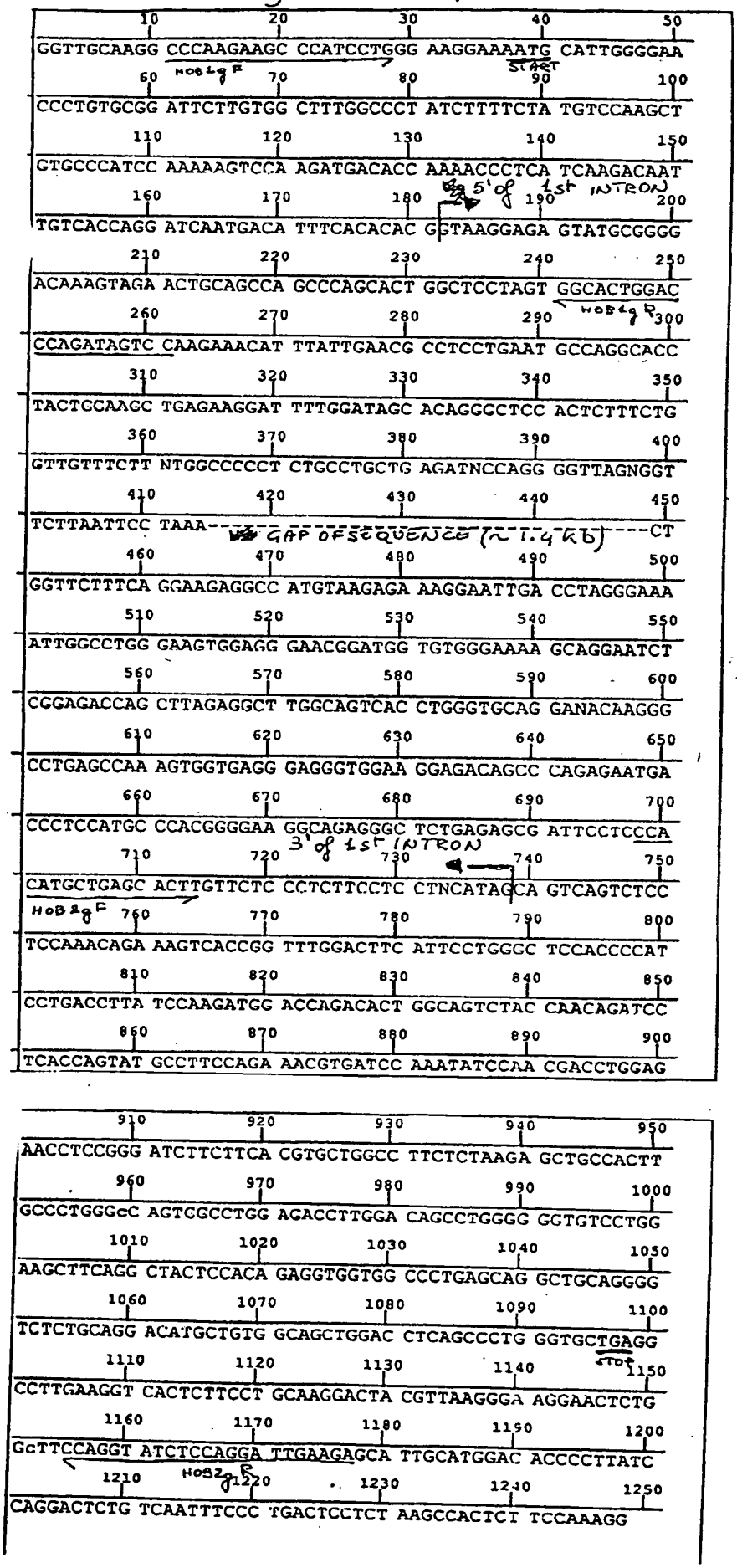

Triton X-100 – – – – +
Proteinase K – – + + +
Microsome – + – + +
preob
ob
31.0 kD
21.5 kD
14.3 kD

Figure 20A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HOB1gF
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110 120 130 140 150
GTGCCCATCC AAAAAGTCCA AGATGACACC AAAACCCTCA TCAAGACAAT
5' of 1st INTRON
160 170 180 190 200
TGTCACCAGG ATCAATGACA TTTCACACAC GGTAAGGAGA GTATGCGGGG
210 220 230 240 250
ACAAAGTAGA ACTGCAGCCA GCCCAGCACT GGCTCCTAGT GGCACTGGAC
HOB1gR
260 270 280 290 300
CCAGATAGTC CAAGAAACAT TTATTGAACG CCTCCTGAAT GCCAGGCACC
310 320 330 340 350
TACTGCAAGC TGAGAAGGAT TTTGGATAGC ACAGGCCTCC ACTCTTTCTG
360 370 380 390 400
GTTGTTTCTT NTGGCCCCCT CTGCCTGCTG AGATNCCAGG GGTTAGNGGT
410 420 430 440 450
TCTTAATTCC TAAA---------- GAP OF SEQUENCE (~1.4 KB) ----------CT
460 470 480 490 500
GGTTCTTTCA GGAAGAGGCC ATGTAAGAGA AAGGAATTGA CCTAGGGAAA
510 520 530 540 550
ATTGGCCTGG GAAGTGGAGG GAACGGATGG TGTGGGAAAA GCAGGAATCT
560 570 580 590 600
CGGAGACCAG CTTAGAGGCT TGGCAGTCAC CTGGGTGCAG GANACAAGGG
610 620 630 640 650
CCTGAGCCAA AGTGGTGAGG GAGGGTGGAA GGAGACAGCC CAGAGAATGA
660 670 680 690 700
CCCTCCATGC CCACGGGGAA GGCAGAGGGC TCTGAGAGCG ATTCCTCCCA
3' of 1st INTRON
710 720 730 740 750
CATGCTGAGC ACTTGTTCTC CCTCTTCCTC CTNCATAGCA GTCAGTCTCC
HOB2gF
760 770 780 790 800
TCCAAACAGA AAGTCACCGG TTTGGACTTC ATTCCTGGGC TCCACCCCAT
810 820 830 840 850
CCTGACCTTA TCCAAGATGG ACCAGACACT GGCAGTCTAC CAACAGATCC
860 870 880 890 900
TCACCAGTAT GCCTTCCAGA AACGTGATCC AAATATCCAA CGACCTGGAG
910 920 930 940 950
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960 970 980 990 1000
GCCCCTGGGcC AGTCGCCTGG AGACCTTGGA CAGCCTGGGG GGTGTCCTGG
1010 1020 1030 1040 1050
AAGCTTCAGG CTACTCCACA GAGGTGGTGG CCCTGAGCAG GCTGCAGGGG
1060 1070 1080 1090 1100
TCTCTGCAGG ACATGCTGTG GCAGCTGGAC CTCAGCCCTG GGTGCTGAGG
STOP
1110 1120 1130 1140 1150
CCTTGAAGGT CACTCTTCCT GCAAGGACTA CGTTAAGGGA AGGAACTCTG
1160 1170 1180 1190 1200
GcTTCCAGGT ATCTCCAGGA TTGAAGAGCA TTGCATGGAC ACCCCTTATC
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Figure 20B

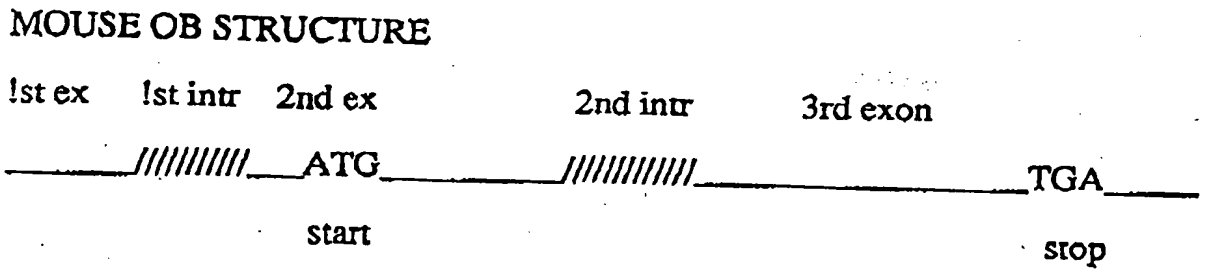

Figure 20c

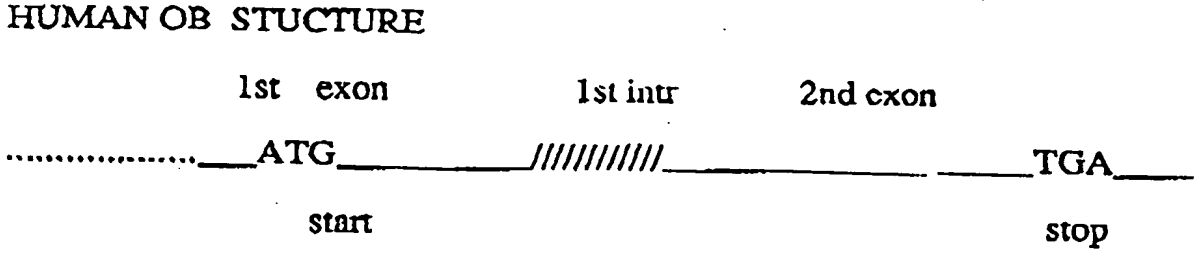

Figure 21A

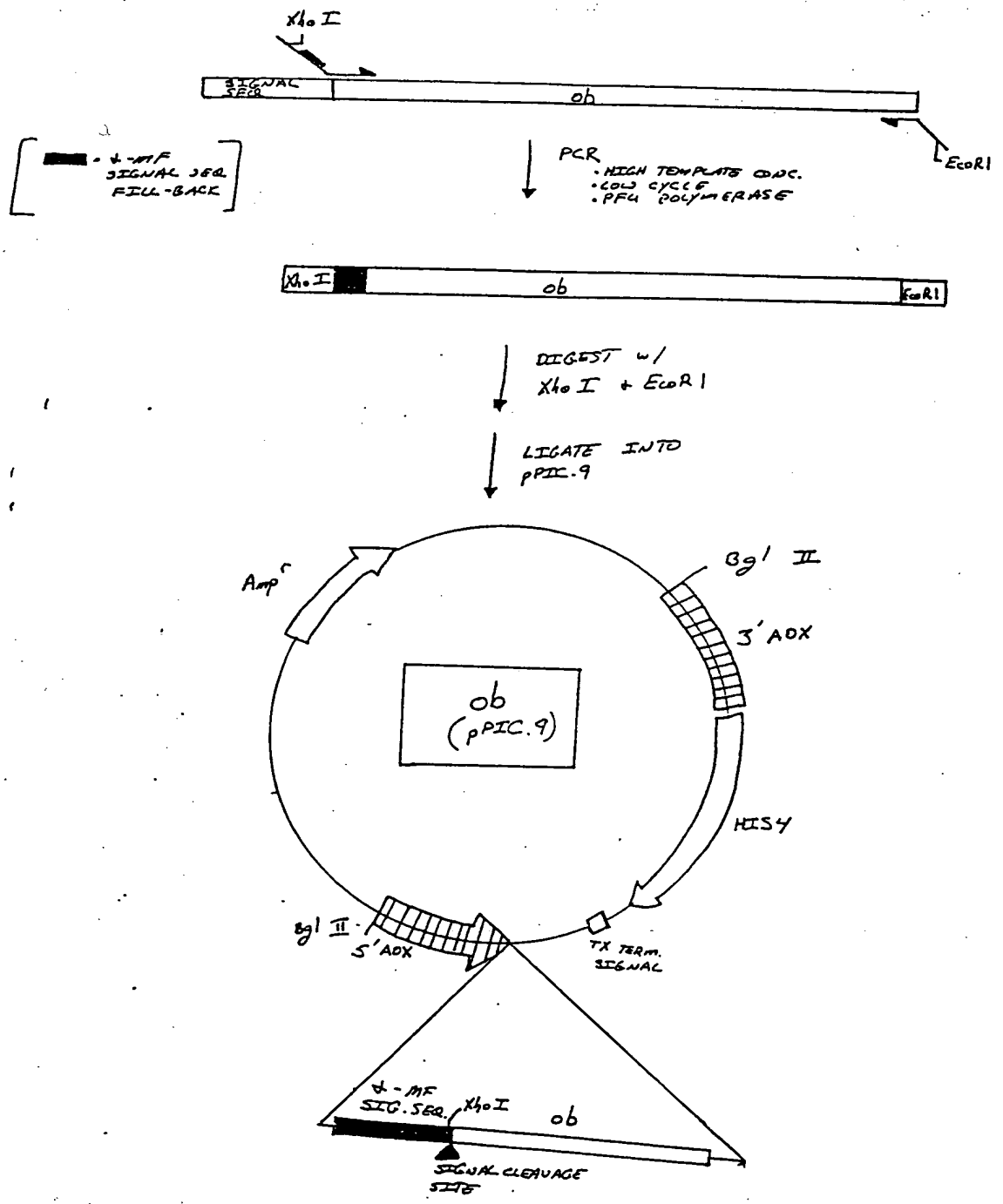
Xho I
SIGNAL SEQ
ob
EcoR I
α-MF SIGNAL SEQ. FILL-BACK
PCR
• HIGH TEMPLATE CONC.
• LOW CYCLE
• PFU POLYMERASE
Xho I
ob
EcoR I
DIGEST w/ Xho I + EcoR I
LIGATE INTO pPIC.9
Amp^r
Bgl II
3' AOX
ob (pPIC.9)
HIS4
Bgl II
5' AOX
TX TERM. SIGNAL
α-MF SIG. SEQ.
Xho I
ob
SIGNAL CLEAVAGE SITE

Figure 21 B

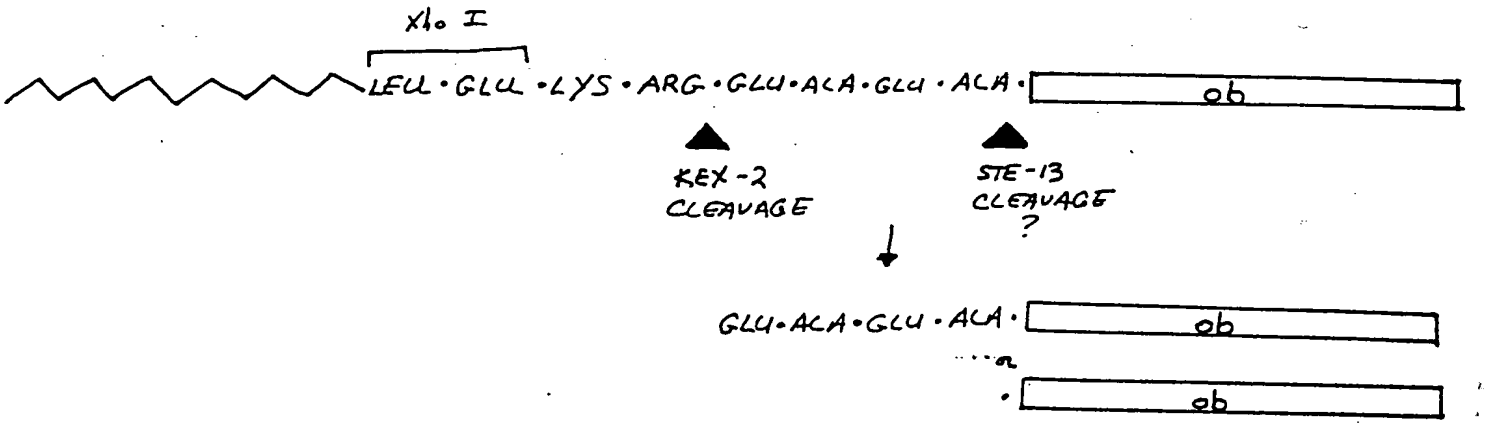

Figure 21 C

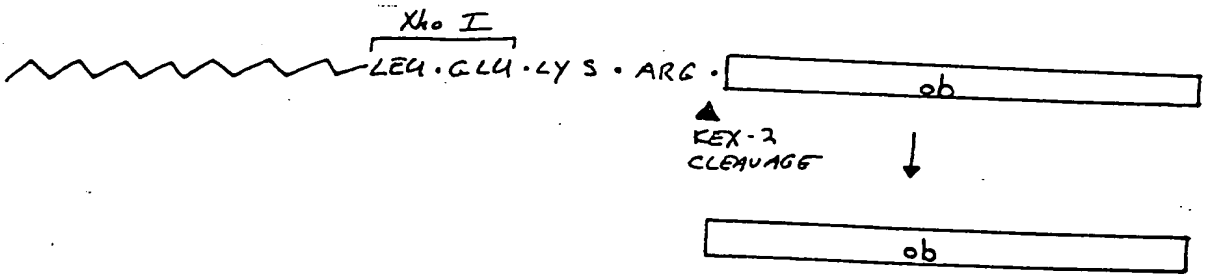

Figure 22A

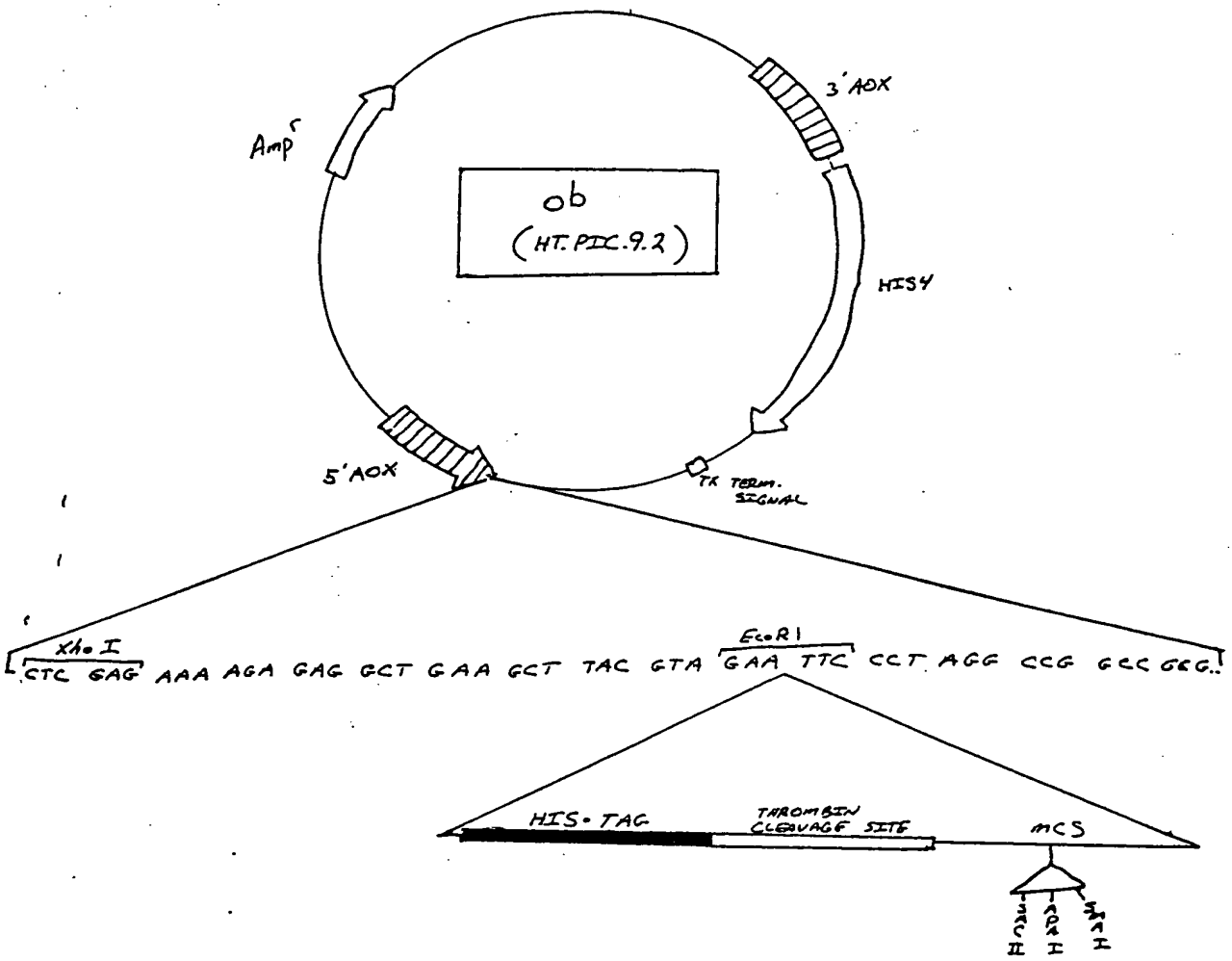
Amp^r
3'AOX
ob
(HT.PIC.9.2)
HIS4
5'AOX
TX TERM. SIGNAL
Xho I
CTC GAG AAA AGA GAG GCT GAA GCT TAC GTA GAA TTC CCT AGG CCG GCC GCG
EcoR I
HIS·TAG
THROMBIN CLEAVAGE SITE
MCS
Sac II
Not I
Xba I

Figure 22B

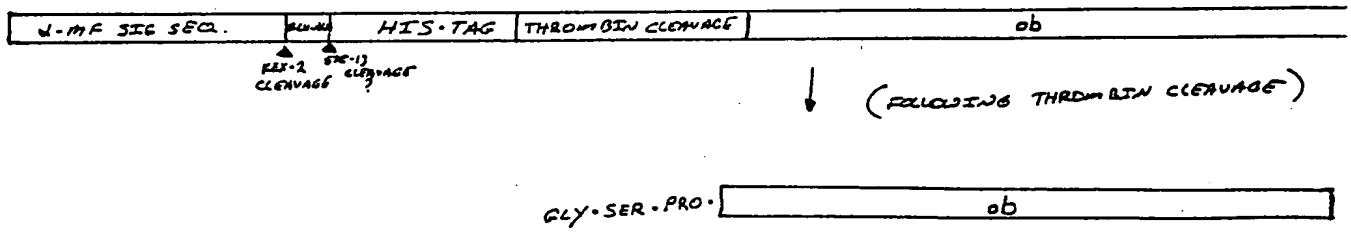
α-MF SIG SEQ.
HIS-TAG
THROMBIN CLEAVAGE
ob
KEX-2 CLEAVAGE
STE-13 CLEAVAGE
(FOLLOWING THROMBIN CLEAVAGE)
GLY-SER-PRO-
ob

Figure 23A.

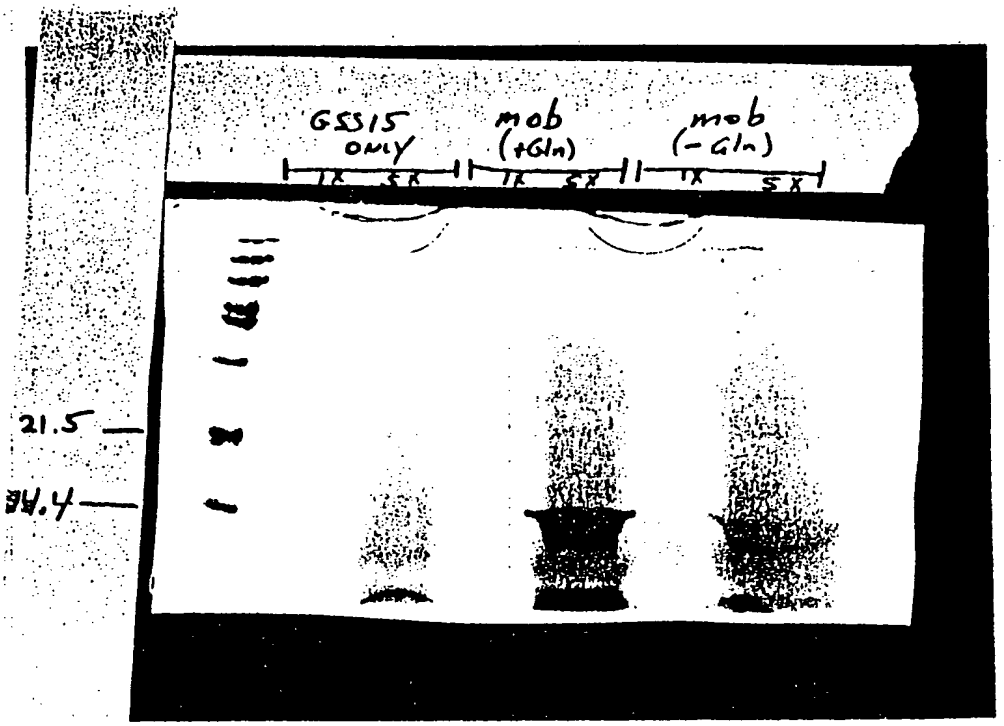

Figure 23B